

OK #5

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/517,155  
Source: PCT  
Date Processed by STIC: 3/31/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 01/10/06



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/517,155

DATE: 03/31/2006  
TIME: 15:12:17

Input Set : A:\211080011U6.TXT  
Output Set: N:\CRF4\03312006\J517155.raw

4 <110> APPLICANT: Chang, Chawnshang  
 6 <120> TITLE OF INVENTION: Androgen Receptor Coregulators  
 9 <130> FILE REFERENCE: 21108.0011U6  
 11 <140> CURRENT APPLICATION NUMBER: 10/517,155  
 C--> 12 <141> CURRENT FILING DATE: 2004-12-06  
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/17937  
 15 <151> PRIOR FILING DATE: 2003-06-06  
 17 <150> PRIOR APPLICATION NUMBER: US 60/387,087  
 18 <151> PRIOR FILING DATE: 2002-06-06  
 20 <160> NUMBER OF SEQ ID NOS: 47  
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1721  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapien  
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 31 <222> LOCATION: (40)...(1464)  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: misc\_feature  
 35 <222> LOCATION: (1120)...(1452)  
 36 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the  
 37 C-terminal domain  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: misc\_feature  
 41 <222> LOCATION: (697)...(834)  
 42 <223> OTHER INFORMATION: Coding sequence and polypeptide region which may  
 43 form a cystein-rich RING finger motif  
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 46 <221> NAME/KEY: misc\_feature  
 47 <222> LOCATION: (964)...(1089)  
 48 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a  
 49 cystein-rich B box like structure  
 51 <400> SEQUENCE: 1  
 52 ggtctctggc ctcccccttc tgagcactct gaggtcctt atg tcg tca gaa gat 54  
 53 Met Ser Ser Glu Asp  
 54 1 5  
 56 cga gaa gct cag gag gat gaa ttg ctg gcc ctg gca agt att tac gat 102  
 57 Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp  
 58 10 15 20  
 60 gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg 150  
 61 Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg  
 62 25 30 35

pp 6-7  
 Does Not Comply  
 Corrected Diskette Needed

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Input Set : A:\211080011U6.TXT  
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64 atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat	198
65 Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn	
66 40 45 50	
68 tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt	246
69 Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe	
70 55 60 65	
72 ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc	294
73 Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser	
74 70 75 80 85	
76 tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act	342
77 Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr	
78 90 95 100	
80 cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac	390
81 Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His	
82 105 110 115	
84 cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag	438
85 Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu	
86 120 125 130	
88 acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt	486
89 Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly	
90 135 140 145	
92 tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca	534
93 Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr	
94 150 155 160 165	
96 gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa	582
97 Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu	
98 170 175 180	
100 att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg	630
101 Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu	
102 185 190 195	
104 atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt	678
105 Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe	
106 200 205 210	
108 aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt	726
109 Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly	
110 215 220 225	
112 agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc	774
113 Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala	
114 230 235 240 245	
116 tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa	822
117 Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln	
118 250 255 260	
120 tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt	870
121 Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly	
122 265 270 275	
124 cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc	918
125 Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg	
126 280 285 290	
128 ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc	966

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Input Set : A:\211080011U6.TXT  
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129 Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys  
 130 295 300 305  
 132 ccc cg<sup>g</sup> cc<sup>g</sup> tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc 1014  
 133 Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr  
 134 310 315 320 325  
 136 atg ggt atc tgc tcc agc tgc aat ttt gcc ttc tgt act ttg tgc agg 1062  
 137 Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg  
 138 330 335 340  
 140 ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta 1110  
 141 Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val Thr Ala Glu Lys Leu  
 142 345 350 355  
 144 atg gac tta cga aat gaa tac ctg caa gcg gat gag gct aat aaa aga 1158  
 145 Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp Glu Ala Asn Lys Arg  
 146 360 365 370  
 148 ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa 1206  
 149 Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu  
 150 375 380 385  
 152 gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca 1254  
 153 Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro  
 154 390 395 400 405  
 156 tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca 1302  
 157 Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr  
 158 410 415 420  
 160 tgt act ggc tgt atg caa tat ttc tgt tgg att tgc atg ggt tct ctc 1350  
 161 Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu  
 162 425 430 435  
 164 tct aga gca aac cct tac aaa cat ttc aat gac cct ggt tca cca tgt 1398  
 165 Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys  
 166 440 445 450  
 168 ttt aac cgg ctg ttt tat gct gtg gat gtt gac gac gat att tgg gaa 1446  
 169 Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp Asp Asp Ile Trp Glu  
 170 455 460 465  
 172 gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg 1494  
 173 Asp Glu Val Glu Asp \*  
 174 470  
 176 ctcaagatat ggaagtggat tg<sup>tttttccc</sup> taatcttccg tcaagtacac aaagtaactt 1554  
 177 tgcggatat ttaggtact attcattcac tcttcctgcg tagaagatat ggaagaacga 1614  
 178 gg<sup>tttatatt</sup> ttcatgtggt actactgaag aaggtgcatt gatacattt taaatgtaa 1674  
 179 ttgagaaaaa ttataagcc aaaggttcag aaaattaaac tacagaa 1721  
 181 <210> SEQ ID NO: 2  
 182 <211> LENGTH: 474  
 183 <212> TYPE: PRT  
 184 <213> ORGANISM: Homo sapien  
 186 <400> SEQUENCE: 2  
 187 Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu  
 188 1 5 10 15  
 189 Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln  
 190 20 25 30  
 191 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile

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192 35 40 45  
193 Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu  
194 50 55 60  
195 Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro  
196 65 70 75 80  
197 Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys  
198 85 90 95  
199 Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn  
200 100 105 110  
201 Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln  
202 115 120 125  
203 Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe  
204 130 135 140  
205 Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln  
206 145 150 155 160  
207 Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp  
208 165 170 175  
209 Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu  
210 180 185 190  
211 Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln  
212 195 200 205  
213 Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe  
214 210 215 220  
215 Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His  
216 225 230 235 240  
217 Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg  
218 245 250 255  
219 Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser  
220 260 265 270  
221 Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe  
222 275 280 285  
223 Ala Arg Tyr Asp Arg Leu Leu Gln Ser Ser Leu Asp Leu Met Ala  
224 290 295 300  
225 Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln  
226 305 310 315 320  
227 Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe  
228 325 330 335  
229 Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val  
230 340 345 350  
231 Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp  
232 355 360 365  
233 Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile  
234 370 375 380  
235 Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn  
236 385 390 395 400  
237 Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly  
238 405 410 415  
239 Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile  
240 420 425 430

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Output Set: N:\CRF4\03312006\J517155.raw

241 Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp  
 242 435 440 445  
 243 Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp  
 244 450 455 460  
 245 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp  
 246 465 470  
 248 <210> SEQ ID NO: 3  
 249 <211> LENGTH: 1335  
 250 <212> TYPE: DNA  
 251 <213> ORGANISM: Homo sapien  
 253 <220> FEATURE:  
 254 <221> NAME/KEY: CDS  
 255 <222> LOCATION: (1)...(1335)  
 257 <220> FEATURE:  
 258 <221> NAME/KEY: misc\_feature  
 259 <222> LOCATION: (750)...(1332)  
 260 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the  
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 263 <220> FEATURE:  
 264 <221> NAME/KEY: misc\_feature  
 265 <222> LOCATION: (631)...(783)  
 266 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a  
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 269 <220> FEATURE:  
 270 <221> NAME/KEY: misc\_feature  
 271 <222> LOCATION: (808)...(996)  
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 275 <220> FEATURE:  
 276 <221> NAME/KEY: misc\_feature  
 277 <222> LOCATION: (985)...(1137)  
 278 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a  
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 281 <220> FEATURE:  
 282 <221> NAME/KEY: misc\_feature  
 283 <222> LOCATION: (1162)...(1314)  
 284 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a  
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 287 <400> SEQUENCE: 3  
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 289 Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr  
 290 1 5 10 15  
 292 cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct 96  
 293 Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser  
 294 20 25 30  
 296 tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag 144  
 297 Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys  
 298 35 40 45  
 300 cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct 192

10/5/77, 195

6

<210> 11  
<211> 32  
<212> PRT  
<213> Homo sapien

<220>  
<221> VARIANT *what about Xaa at location 5?*  
<222> 2-3, 6-13, 15, 17-18, 20-21, 23-28, 30-31  
<223> Xaa can be any amino acid

<400> 11  
Cys Xaa Xaa Cys (Xaa) Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa His  
1 5 10 15  
Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys  
20 25 30

7  
RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/517,155

DATE: 03/31/2006  
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Input Set : A:\211080011U6.TXT  
Output Set: N:\CRF4\03312006\J517155.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,(5),6,7,8,9,10,11,12,13,15,17,18,20,21,23,24,25,26,27

Seq#:11; Xaa Pos. 28,30,31

Seq#:12; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,22,23,25

Seq#:12; Xaa Pos. 26,28,29,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46

Seq#:12; Xaa Pos. 48,49

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/517,155

DATE: 03/31/2006  
TIME: 15:12:18

Input Set : A:\211080011U6.TXT  
Output Set: N:\CRF4\03312006\J517155.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
M:341 Repeated in SeqNo=11  
L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
M:341 Repeated in SeqNo=12